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OM protein - protein search, using sw model

Run on: November 17, 2005, 22:29:18 ; Search time 75 Seconds
(without alignments)
72.195 Million cell updates/sec

Title: US-09-745-008-14
Perfect score: 78
Sequence: 1 RQRLPKRMGGSYRC 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	100.0	14	ADC21513	Adc21513 T. cruzi
2	78	100.0	21	ADC21512	Adc21512 T. cruzi
3	78	100.0	1162	ADC21533	Adc21533 T. cruzi
4	67.5	86.5	45	ADC21511	Adc21511 T. cruzi
5	45	57.7	433	ABO79949	ABO79949 Pseudomon
6	43	55.1	164	ABO81408	ABO81408 Pseudomon
7	43	55.1	164	ABO71869	ABO71869 Pseudomon
8	43	55.1	223	ABO70073	ABO70073 Pseudomon
9	43	55.1	545	ABO81671	ABO81671 Pseudomon
10	42.5	54.5	1107	ABO62373	ABO62373 Klebsiell
11	42	53.8	30	AAW89049	AAW89049 Polypepti
12	42	53.8	30	ABB51214	ABB51214 Human sec
13	42	53.8	30	ABO45471	ABO45471 Novel hum
14	42	53.8	30	ABO26951	ABO26951 Protein a
15	42	53.8	339	ABB68550	ABB68550 Drosophil
16	42	53.8	419	ABO68753	ABO68753 Pseudomon
17	41	52.6	189	AAU42341	AAU42341 Propionib
18	41	52.6	189	ABM38860	ABM38860 Propionib
19	41	52.6	212	ABB75629	ABB75629 Human end
20	41	52.6	492	ABO71785	ABO71785 Pseudomon
21	41	52.6	511	ABO69945	ABO69945 Pseudomon
22	41	52.6	556	ABO73842	ABO73842 Pseudomon
23	41	52.6	564	ADN17932	ADN17932 Bacterial
24	41	52.6	595	ABO68723	ABO68723 Pseudomon
25	40.5	51.9	235	AAR05328	AAR05328 Rat tumou

26	40.5	51.9	235	2	AAR05996	Aar05996 Rat tumou
27	40.5	51.9	235	5	AAU10546	Aau10546 Rat tumou
28	40	51.3	61	8	ADO47390	Ado47390 Human neu
29	40	51.3	92	3	AAG33234	Aag33234 Zea mays
30	40	51.3	138	3	AAG33233	Aag33233 Zea mays
31	40	51.3	151	4	ABG16755	Abg16755 Novel hum
32	40	51.3	230	4	AAG98324	Aag98324 Escherich
33	40	51.3	230	6	ABU14845	Abu14845 Protein e
34	40	51.3	259	7	ADB64149	Adb64149 Human pro
35	40	51.3	279	7	ABM74436	Abm74436 DNA clone
36	40	51.3	299	4	ABB76024	Abb76024 Human pro
37	40	51.3	299	8	ADO47379	Ado47379 Human neu
38	40	51.3	302	6	ABU52331	Abu52331 Human GPC
39	40	51.3	302	6	ABU52330	Abu52330 Human NOV
40	40	51.3	302	8	ADL23995	Adl23995 Human NOV
41	40	51.3	302	8	ADL23997	Adl23997 Human NOV
42	40	51.3	303	7	ABO74011	AbO74011 Pseudomon
43	40	51.3	355	7	ABO78680	AbO78680 Pseudomon
44	40	51.3	362	7	ABO81880	AbO81880 Pseudomon
45	40	51.3	419	7	ABO79741	AbO79741 Pseudomon

ALIGNMENTS

RESULT 1

ADC21513
ID ADC21513 standard; peptide; 14 AA.

XX AC ADC21513;

XX DT 18-DEC-2003 (first entry)

XX DE T. cruzi trans-sialidase, TS, neurotrophic peptide C14.

XX KW Trans-sialidase; TS; neurotrophic peptide; interleukin-6;

KW IL-6 secretion inducing peptide; neuron; glial cell; trophic support;

KW ciliary neurotrophic factor; CNTF; leukaemia inhibitory factor; LIF;

KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;

KW Huntington's disease; Chagas' disease; peripheral neuropathy; palsy;

KW multiple sclerosis; stroke; brain trauma; spinal cord trauma;

KW peripheral nerve trauma.

XX OS Trypanosoma cruzi.

XX PN US2002137667-A1.

XX PD 26-SEP-2002.

XX PF 20-DEC-2000; 2000US-00745008.

XX PR 20-DEC-1999; 99US-0172881P.

XX PA (TUFT) UNIV TUFTS.

XX PI Chuenkova M, Pereira MA;

XX DR WPI; 2003-786654/74.

XX PT T. cruzi trans-sialidase derived neurotrophic and interleukin-6 secretion inducing peptides, useful in the treatment of neuronal degeneration caused for example by Chagas' disease.

XX PS Claim 5; SEQ ID NO 14; 79pp; English.

XX CC The invention relates to a T. cruzi trans-sialidase (TS) derived neurotrophic peptide appearing as ADC21513 or ADC21511 called C44 and C14, or its variant, and an interleukin-6 (IL-6) secretion inducing peptide appearing as ADC21511 called TR-1 (terminal repeat 1). Also included are a composition comprising the peptides, fusion protein comprising the peptides and a fusion partner, a composition comprising the fusion protein and a physiological acceptable carrier, providing trophic support for neurons or glial cells in a mammal (comprising

CC administering a therapeutically effective amount of T. cruzi trans-
CC sialidase (TS) or a neurotrophic variant) and stimulating (M3) the
CC secretion of IL-6 (interleukin-6) in a mammal comprising administering TS
CC or an IL-6 inducing variant. The fusion partner comprises a mammalian
CC neurotrophic factor which is ciliary neurotrophic factor (CNTF) or
CC leukaemia inhibitory factor (LIF). The peptides are useful in providing
CC trophic support for neurons and glial cells in a mammal suffering a
CC condition selected from: amyotrophic lateral sclerosis, Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, Chagas' disease,
CC peripheral neuropathy, palsies, multiple sclerosis, stroke, brain trauma,
CC spinal cord trauma and peripheral nerve trauma, and in stimulating the
CC secretion of IL-6. The present sequence represents a trans-sialidase
CC neurotrophic peptide.

XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 78; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRLPKRMGGSYRC 14
|||||
Db 1 RQRLPKRMGGSYRC 14

RESULT 2

ADC21512
ID ADC21512 standard; peptide; 21 AA.

XX
AC ADC21512;

XX
DT 18-DEC-2003 (first entry)

XX
DE T. cruzi trans-sialidase, TS, neurotrophic peptide CFN1.

XX
KW Trans-sialidase; TS; neurotrophic peptide; interleukin-6;
KW IL-6 secretion inducing peptide; neuron; glial cell; trophic support;
KW ciliary neurotrophic factor; CNTF; leukaemia inhibitory factor; LIF;
KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; Chagas' disease; peripheral neuropathy; palsy;
KW multiple sclerosis; stroke; brain trauma; spinal cord trauma;
KW peripheral nerve trauma.

XX
OS Trypanosoma cruzi.

XX
PN US2002137667-A1.

XX
PD 26-SEP-2002.

XX
PF 20-DEC-2000; 2000US-00745008.

XX
PR 20-DEC-1999; 99US-0172881P.

XX
PA (TUFT) UNIV TUFTS.

XX
PI Chuenkova M, Pereira MA;

XX
DR WPI; 2003-786654/74.

XX
PT T. cruzi trans-sialidase derived neurotrophic and interleukin-6 secretion
PT inducing peptides, useful in the treatment of neuronal degeneration
PT caused for example by Chagas' disease.

XX
PS Example 1; SEQ ID NO 13; 79pp; English.

XX
CC The invention relates to a T. cruzi trans-sialidase (TS) derived
CC neurotrophic peptide appearing as ADC21513 or ADC21511 called C44 and
CC C14, or its variant, and an interleukin-6 (IL-6) secretion inducing
CC peptide appearing as ADC21531 called TR-1 (terminal repeat 1). Also
CC included are a composition comprising the peptides, fusion protein
CC comprising the peptides and a fusion partner, a composition comprising
CC the fusion protein and a physiological acceptable carrier, providing
CC trophic support for neurons or glial cells in a mammal (comprising

CC administering a therapeutically effective amount of T. cruzi trans-
CC sialidase (TS) or a neurotrophic variant) and stimulating (M3) the
CC secretion of IL-6 (interleukin-6) in a mammal comprising administering TS
CC or an IL-6 inducing variant. The fusion partner comprises a mammalian
CC neurotrophic factor which is ciliary neurotrophic factor (CNTF) or
CC leukaemia inhibitory factor (LIF). The peptides are useful in providing
CC trophic support for neurons and glial cells in a mammal suffering a
CC condition selected from: amyotrophic lateral sclerosis, Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, Chagas' disease,
CC peripheral neuropathy, palsies, multiple sclerosis, stroke, brain trauma,
CC spinal cord trauma and peripheral nerve trauma, and in stimulating the
CC secretion of IL-6. The present sequence represents a trans-sialidase
CC neurotrophic peptide.

XX
SQ Sequence 21 AA;

Query Match 100.0%; Score 78; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRLPKRMGGSYRC 14
|||||
Db 1 RQRLPKRMGGSYRC 14

RESULT 3

ADC21533
ID ADC21533 standard; protein; 1162 AA.

XX
AC ADC21533;

XX
DT 18-DEC-2003 (first entry)

XX
DE T. cruzi trans-sialidase, TS, clone 7P.

XX
KW Trans-sialidase; TS; neurotrophic peptide; interleukin-6;
KW IL-6 secretion inducing peptide; neuron; glial cell; trophic support;
KW ciliary neurotrophic factor; CNTF; leukaemia inhibitory factor; LIF;
KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; Chagas' disease; peripheral neuropathy; palsy;
KW multiple sclerosis; stroke; brain trauma; spinal cord trauma;
KW peripheral nerve trauma.

XX
OS Trypanosoma cruzi.

XX
PN US2002137667-A1.

XX
PD 26-SEP-2002.

XX
PF 20-DEC-2000; 2000US-00745008.

XX
PR 20-DEC-1999; 99US-0172881P.

XX
PA (TUFT) UNIV TUFTS.

XX
PI Chuenkova M, Pereira MA;

XX
DR WPI; 2003-786654/74.

XX
PT T. cruzi trans-sialidase derived neurotrophic and interleukin-6 secretion
PT inducing peptides, useful in the treatment of neuronal degeneration
PT caused for example by Chagas' disease.

XX
PS Disclosure; SEQ ID NO 34; 79pp; English.

XX
CC The invention relates to a T. cruzi trans-sialidase (TS) derived
CC neurotrophic peptide appearing as ADC21513 or ADC21511 called C44 and
CC C14, or its variant, and an interleukin-6 (IL-6) secretion inducing
CC peptide appearing as ADC21531 called TR-1 (terminal repeat 1). Also
CC included are a composition comprising the peptides, fusion protein
CC comprising the peptides and a fusion partner, a composition comprising
CC the fusion protein and a physiological acceptable carrier, providing
CC the fusion protein and a physiological acceptable carrier, providing

CC trophic support for neurons or glial cells in a mammal (comprising
CC administering a therapeutically effective amount of T. cruzi trans-
CC sialidase (TS) or a neurotrophic variant) and stimulating (M3) the
CC secretion of IL-6 (interleukin-6) in a mammal comprising administering TS
CC or an IL-6 inducing variant. The fusion partner comprises a mammalian
CC neurotrophic factor which is ciliary neurotrophic factor (CNTF) or
CC leukaemia inhibitory factor (LIF). The peptides are useful in providing
CC trophic support for neurons and glial cells in a mammal suffering a
CC condition selected from: amyotrophic lateral sclerosis, Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, Chagas' disease,
CC peripheral neuropathy, palsies, multiple sclerosis, stroke, brain trauma,
CC spinal cord trauma and peripheral nerve trauma, and in stimulating the
CC secretion of IL-6. The present sequence represents trans-sialidase clone
CC 7F.

XX
SQ Sequence 1162 AA;

Query Match 100.0%; Score 78; DB 7; Length 1162;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRLPKRMGGSYRC 14
|||||
Db 379 RQRLPKRMGGSYRC 392

RESULT 4

ADC21511
ID ADC21511 standard; peptide; 45 AA.

XX
AC ADC21511;

DT 18-DEC-2003 (first entry)

DE T. cruzi trans-sialidase, TS, neurotrophic peptide C44.

XX
KW Trans-sialidase; TS; neurotrophic peptide; interleukin-6;
KW IL-6 secretion inducing peptide; neuron; glial cell; trophic support;
KW ciliary neurotrophic factor; CNTF; leukaemia inhibitory factor; LIF;
KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; Chagas' disease; peripheral neuropathy; palsy;
KW multiple sclerosis; stroke; brain trauma; spinal cord trauma;
KW peripheral nerve trauma.

XX Trypanosoma cruzi.

OS US2002137667-A1.

PN
XX
XX
PD 26-SEP-2002.

XX
PF 20-DEC-2000; 2000US-00745008.

XX
PR 20-DEC-1999; 99US-0172881P.

XX (TUFT) UNIV TUFTS.

XX Chuenkova M, Pereira MA;

XX WPI; 2003-786654/74.

XX
PT T. cruzi trans-sialidase derived neurotrophic and interleukin-6 secretion
PT inducing peptides, useful in the treatment of neuronal degeneration
PT caused for example by Chagas' disease.

XX Claim 4; SEQ ID NO 12; 79pp; English.

XX The invention relates to a T. cruzi trans-sialidase (TS) derived
CC neurotrophic peptide appearing as ADC21513 or ADC21511 called C44 and
CC C14, or its variant, and an interleukin-6 (IL-6) secretion inducing
CC peptide appearing as ADC21531 called TR-1 (terminal repeat 1). Also
CC included are a composition comprising the peptides, fusion protein
CC comprising the peptides and a fusion partner, a composition comprising
CC the fusion protein and a physiological acceptable carrier, providing

CC trophic support for neurons or glial cells in a mammal (comprising
CC administering a therapeutically effective amount of T. cruzi trans-
CC sialidase (TS) or a neurotrophic variant) and stimulating (M3) the
CC secretion of IL-6 (interleukin-6) in a mammal comprising administering TS
CC or an IL-6 inducing variant. The fusion partner comprises a mammalian
CC neurotrophic factor which is ciliary neurotrophic factor (CNTF) or
CC leukaemia inhibitory factor (LIF). The peptides are useful in providing
CC trophic support for neurons and glial cells in a mammal suffering a
CC condition selected from: amyotrophic lateral sclerosis, Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, Chagas' disease,
CC peripheral neuropathy, palsies, multiple sclerosis, stroke, brain trauma,
CC spinal cord trauma and peripheral nerve trauma, and in stimulating the
CC secretion of IL-6. The present sequence represents a trans-sialidase
CC neurotrophic peptide.

XX
SQ Sequence 45 AA;

Query Match 86.5%; Score 67.5; DB 7; Length 45;
Best Local Similarity 93.3%; Pred. No. 0.00028;
Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 RQRLP-KRMGGSYRC 14
|||||
Db 24 RQRLP-KRMGGSYRC 38

RESULT 5

ABO79949

ID ABO79949 standard; protein; 433 AA.

XX
AC ABO79949;

DT 29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polypeptide #12124.

XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX Pseudomonas aeruginosa.

OS
XX US6551795-B1.

PN 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

PR 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

DR WPI; 2003-615309/58.

DR N-PSDB; ABD13520.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 28695; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences

CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 433 AA;

Query Match 57.7%; Score 45; DB 7; Length 433;
Best Local Similarity 64.3%; Pred. No. 28;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 RQRLPKRMGGSYRC 14
Db 251 RRLPVRPGGPGRC 264
|:|:|:|:|:|:|

RESULT 6
ABO81408
ID ABO81408 standard; protein; 164 AA.
XX
AC ABO81408;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #13583.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR N-PSDB; ABD14979.

XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 164 AA;

Query Match 55.1%; Score 43; DB 7; Length 164;

Best Local Similarity 50.0%; Pred. No. 24;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 RQRLPKRMGGSYRC 14
Db 73 RRRMPRRSGPATRC 86
|:|:|:|:|:|:|

RESULT 7
ABO71869
ID ABO71869 standard; protein; 164 AA.
XX
AC ABO71869;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #4044.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR N-PSDB; ABD05440.

XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 164 AA;

Query Match 55.1%; Score 43; DB 7; Length 164;

Best Local Similarity 50.0%; Pred. No. 24;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 RQRLPKRMGGSYRC 14
Db 73 RRRMPRRSGPATRC 86
|:|:|:|:|:|:|

RESULT 8

PF 27-JAN-2000; 2000US-00489039.
XX
PR 29-JAN-1999; 99US-0117747P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
XX Breton GL, Osborne M;
PI
XX WPI; 2003-895346/82.
DR N-PSDB; ACH95924.
XX
PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.
XX
PS Disclosure; SEQ ID NO 8890; 932pp; English.
XX
CC The invention describes a new isolated nucleic acid encoding a Klebsiella
CC pneumoniae polypeptide. Also described are: a recombinant expression
CC vector comprising the nucleic acid, operably linked to a transcription
CC regulatory element; and a cell comprising the recombinant expression
CC vector. The nucleic acid is useful for preparing a vaccine composition
CC against Klebsiella pneumoniae. This is the amino acid sequence of a
CC Klebsiella pneumoniae polypeptide of the invention
XX
SQ Sequence 1107 AA;

Query Match 54.5%; Score 42.5; DB 7; Length 1107;
Best Local Similarity 64.3%; Pred. No. 2.1e+02;
Matches 9; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 RQR-LPKRMGGSYR 13
|||:|:|:|
Db 19 RQRPVDRLLGGQYR 32

RESULT 11
AAW89049
ID AAW89049 standard; protein; 30 AA.
XX
AC AAW89049;
XX
DT 01-MAR-1999 (first entry)
XX
DE Polypeptide fragment encoded by gene 183.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9854963-A2.
XX
PD 10-DEC-1998.
XX
PF 04-JUN-1998; 98WO-US011422.
XX
PR 06-JUN-1997; 97US-0048875P.
PR 06-JUN-1997; 97US-0048876P.
PR 06-JUN-1997; 97US-0048877P.
PR 06-JUN-1997; 97US-0048878P.
PR 06-JUN-1997; 97US-0048880P.
PR 06-JUN-1997; 97US-0048881P.
PR 06-JUN-1997; 97US-0048882P.
PR 06-JUN-1997; 97US-0048883P.
PR 06-JUN-1997; 97US-0048884P.
PR 06-JUN-1997; 97US-0048885P.
PR 06-JUN-1997; 97US-0048892P.

PR 06-JUN-1997; 97US-0048893P.
PR 06-JUN-1997; 97US-0048894P.
PR 06-JUN-1997; 97US-0048895P.
PR 06-JUN-1997; 97US-0048896P.
PR 06-JUN-1997; 97US-0048897P.
PR 06-JUN-1997; 97US-0048898P.
PR 06-JUN-1997; 97US-0048899P.
PR 06-JUN-1997; 97US-0048900P.
PR 06-JUN-1997; 97US-0048901P.
PR 06-JUN-1997; 97US-0048915P.
PR 06-JUN-1997; 97US-0048916P.
PR 06-JUN-1997; 97US-0048917P.
PR 06-JUN-1997; 97US-0048949P.
PR 06-JUN-1997; 97US-0048962P.
PR 06-JUN-1997; 97US-0048963P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048970P.
PR 06-JUN-1997; 97US-0048971P.
PR 06-JUN-1997; 97US-0048972P.
PR 06-JUN-1997; 97US-0048974P.
PR 06-JUN-1997; 97US-0049019P.
PR 06-JUN-1997; 97US-0049020P.
PR 06-JUN-1997; 97US-0049373P.
PR 06-JUN-1997; 97US-0049374P.
PR 06-JUN-1997; 97US-0049375P.
PR 05-SEP-1997; 97US-0057584P.
PR 05-SEP-1997; 97US-0057627P.
PR 05-SEP-1997; 97US-0057628P.
PR 05-SEP-1997; 97US-0057629P.
PR 05-SEP-1997; 97US-0057634P.
PR 05-SEP-1997; 97US-0057635P.
PR 05-SEP-1997; 97US-0057642P.
PR 05-SEP-1997; 97US-0057643P.
PR 05-SEP-1997; 97US-0057644P.
PR 05-SEP-1997; 97US-0057645P.
PR 05-SEP-1997; 97US-0057646P.
PR 05-SEP-1997; 97US-0057647P.
PR 05-SEP-1997; 97US-0057648P.
PR 05-SEP-1997; 97US-0057649P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057651P.
PR 05-SEP-1997; 97US-0057654P.
PR 05-SEP-1997; 97US-0057661P.
PR 05-SEP-1997; 97US-0057662P.
PR 05-SEP-1997; 97US-0057666P.
PR 05-SEP-1997; 97US-0057667P.
PR 05-SEP-1997; 97US-0057668P.
PR 05-SEP-1997; 97US-0057760P.
PR 05-SEP-1997; 97US-0057761P.
PR 05-SEP-1997; 97US-0057762P.
PR 05-SEP-1997; 97US-0057763P.
PR 05-SEP-1997; 97US-0057764P.
PR 05-SEP-1997; 97US-0057765P.
PR 05-SEP-1997; 97US-0057769P.
PR 05-SEP-1997; 97US-0057770P.
PR 05-SEP-1997; 97US-0057771P.
PR 05-SEP-1997; 97US-0057774P.
PR 05-SEP-1997; 97US-0057775P.
PR 05-SEP-1997; 97US-0057776P.
PR 05-SEP-1997; 97US-0057777P.
PR 05-SEP-1997; 97US-0057778P.
PR 18-DEC-1997; 97US-0070923P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Young P, Greene JM, Ferrie AM, Ruben SM, Rosen CA, Hu J;
PI Olsen HS, Ebner R, Brewer LA, Moore PA, Shi Y, Florence C;
PI Florence K, Lafleur DW, Ni J, Fan P, Wei Y, Fischer CL, Soppet DR;
PI Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon PJ, Endress GA;
PI Carter KC;
XX
DR WPI; 1999-059865/05.
DR N-PSDB; AAV84593.

PN US2003065160-A1.
XX
PD 03-APR-2003.
XX
PF 07-DEC-2001; 2001US-00004860.
XX
PR 06-JUN-1997; 97US-0048875P.
PR 06-JUN-1997; 97US-0048876P.
PR 06-JUN-1997; 97US-0048877P.
PR 06-JUN-1997; 97US-0048878P.
PR 06-JUN-1997; 97US-0048880P.
PR 06-JUN-1997; 97US-0048881P.
PR 06-JUN-1997; 97US-0048882P.
PR 06-JUN-1997; 97US-0048883P.
PR 06-JUN-1997; 97US-0048884P.
PR 06-JUN-1997; 97US-0048885P.
PR 06-JUN-1997; 97US-0048892P.
PR 06-JUN-1997; 97US-0048893P.
PR 06-JUN-1997; 97US-0048894P.
PR 06-JUN-1997; 97US-0048895P.
PR 06-JUN-1997; 97US-0048896P.
PR 06-JUN-1997; 97US-0048897P.
PR 06-JUN-1997; 97US-0048898P.
PR 06-JUN-1997; 97US-0048899P.
PR 06-JUN-1997; 97US-0048900P.
PR 06-JUN-1997; 97US-0048901P.
PR 06-JUN-1997; 97US-0048915P.
PR 06-JUN-1997; 97US-0048916P.
PR 06-JUN-1997; 97US-0048917P.
PR 06-JUN-1997; 97US-0048949P.
PR 06-JUN-1997; 97US-0048962P.
PR 06-JUN-1997; 97US-0048963P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048970P.
PR 06-JUN-1997; 97US-0048971P.
PR 06-JUN-1997; 97US-0048972P.
PR 06-JUN-1997; 97US-0048974P.
PR 06-JUN-1997; 97US-0049019P.
PR 06-JUN-1997; 97US-0049020P.
PR 06-JUN-1997; 97US-0049373P.
PR 06-JUN-1997; 97US-0049374P.
PR 06-JUN-1997; 97US-0049375P.
PR 05-SEP-1997; 97US-0057584P.
PR 05-SEP-1997; 97US-0057627P.
PR 05-SEP-1997; 97US-0057628P.
PR 05-SEP-1997; 97US-0057629P.
PR 05-SEP-1997; 97US-0057634P.
PR 05-SEP-1997; 97US-0057635P.
PR 05-SEP-1997; 97US-0057642P.
PR 05-SEP-1997; 97US-0057643P.
PR 05-SEP-1997; 97US-0057644P.
PR 05-SEP-1997; 97US-0057645P.
PR 05-SEP-1997; 97US-0057646P.
PR 05-SEP-1997; 97US-0057647P.
PR 05-SEP-1997; 97US-0057648P.
PR 05-SEP-1997; 97US-0057649P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057651P.
PR 05-SEP-1997; 97US-0057654P.
PR 05-SEP-1997; 97US-0057661P.
PR 05-SEP-1997; 97US-0057662P.
PR 05-SEP-1997; 97US-0057666P.
PR 05-SEP-1997; 97US-0057667P.
PR 05-SEP-1997; 97US-0057668P.
PR 05-SEP-1997; 97US-0057760P.
PR 05-SEP-1997; 97US-0057761P.
PR 05-SEP-1997; 97US-0057762P.
PR 05-SEP-1997; 97US-0057763P.
PR 05-SEP-1997; 97US-0057764P.
PR 05-SEP-1997; 97US-0057765P.
PR 05-SEP-1997; 97US-0057769P.
PR 05-SEP-1997; 97US-0057770P.
PR 05-SEP-1997; 97US-0057771P.

PR 05-SEP-1997; 97US-0057774P.
PR 05-SEP-1997; 97US-0057775P.
PR 05-SEP-1997; 97US-0057776P.
PR 05-SEP-1997; 97US-0057777P.
PR 05-SEP-1997; 97US-0057778P.
PR 18-DEC-1997; 97US-0070923P.
PR 04-JUN-1998; 98WO-US011422.
PR 15-JUL-1998; 98US-0092921P.
PR 30-JUL-1998; 98US-0094657P.
PR 04-DEC-1998; 98US-00205258.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Young P, Greene JM, Ferrie AM, Ruben SM, Rosen CA, Hu J;
PI Olsen HS, Ebner R, Brewer LA, Moore PA, Shi Y, Florence C;
PI Florence K, Lafleur DW, Ni J, Fan P, Wei Y, Fischer CL, Soppet DR;
PI Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon PJ, Endress GA;
PI Carter KC;
XX
DR WPI; 2003-540804/51.
XX
PT New isolated protein, useful for preparing a composition for diagnosing
PT or treating cancer, inflammatory, immune or infectious diseases.
XX
PS Disclosure; Page 112; 172pp; English.
XX
CC The invention relates to an isolated HEMA80 protein. The protein is
CC useful for preparing a composition for diagnosing or treating autoimmune
CC disorders e.g. multiple sclerosis and systemic lupus erythematosus;
CC haematopoietic cell disorders e.g. agammaglobulinaemia and ataxia
CC telangiectasia; blood coagulation disorders e.g. afibrinogenaemia and
CC thrombocytopenia; allergy; graft-versus-host disease; inflammatory
CC conditions e.g. ischaemia-reperfusion injury and arthritis;
CC hyperproliferative disorders e.g. cancer and purpura; infectious disease
CC e.g. viral infection and bacterial infection. The polynucleotide or
CC protein can be used to regenerate damaged tissue e.g. ulcers and
CC Alzheimer's disease. The present sequence represents the amino acid
CC sequence of a novel human secreted protein fragment. Note: The sequence
CC data for this patent did not form part of the printed specification but
CC was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030065160
XX
SQ Sequence 30 AA;

Query Match 53.8%; Score 42; DB 6; Length 30;
Best Local Similarity 61.5%; Pred. No. 6.2;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RQRLPKRMGGSYR 13
 |||:|:|:
Db 5 RQRRPRRRGGTSR 17

RESULT 14
ABO26951
ID ABO26951 standard; protein; 30 AA.
XX
AC ABO26951;
XX
DT 10-SEP-2003 (first entry)
XX
DE Protein associated with novel secreted protein gene 183 #3.
XX
KW Secreted protein; precerebellin-like protein; sepsis; acne; psoriasis;
KW neurodegenerative disorder; behavioural disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; schizophrenia; mania;
KW dementia; paranoia; psychosis; autism; immune disorder; infection;
KW inflammation; allergy; liver disorder; hepatoblastoma; jaundice;
KW hepatitis; immunological disorder; AIDS; leukaemia; rheumatoid arthritis;
cancer.
XX
OS Unidentified.
XX

[illegible]

XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
XX PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL12653.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 32442; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 339 AA;

Query Match 53.8%; Score 42; DB 4; Length 339;
Best Local Similarity 70.0%; Pred. No. 75;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PKRMGGSYRC 14
| | | | |
Db 208 PKRVPGPYRC 217

Search completed: November 18, 2005, 00:27:53
Job time : 81 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model.

Run on: November 17, 2005, 22:32:53 ; Search time 23 Seconds
(without alignments)
58.567 Million cell updates/sec

Title: US-09-745-008-14
Perfect score: 78
Sequence: 1 RQRLPKRMGGSYRC 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: Pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	1162	2 JH0557	exo-alpha-sialidas
2	41	52.6	83	2 AE1851	hypothetical prote
3	41	52.6	564	2 H75403	glycosyl hydrolase
4	40.5	51.9	235	2 JU0029	tumor necrosis fac
5	40	51.3	230	2 G65067	hypothetical prote
6	40	51.3	230	2 B85937	hypothetical prote
7	40	51.3	230	2 G91091	hypothetical prote
8	40	51.3	261	2 JQ0137	hypothetical 30.1K
9	40	51.3	314	2 F75504	probable pilin, ty
10	40	51.3	428	2 H86890	hypothetical prote
11	40	51.3	538	2 T51756	NAD+ synthase (glu
12	40	51.3	1559	2 T07757	probable DNA (cyto
13	39	50.0	298	2 B71013	hypothetical prote
14	39	50.0	332	2 G81395	probable ATP /GTP
15	39	50.0	372	2 C90498	carnitine dehydrat
16	39	50.0	395	2 A96215	hypothetical prote
17	39	50.0	395	2 AH3071	conserved hypothet
18	39	50.0	472	2 T50637	probable histidine
19	39	50.0	520	2 S11217	viropilamin - caul
20	39	50.0	1638	2 D87749	protein unc-73b [i
21	39	50.0	1677	2 T14267	xin protein, stage
22	39	50.0	2488	2 T42739	guanine nucleotide
23	38	48.7	210	2 S28673	hypothetical prote
24	38	48.7	356	2 F95954	probable dTDPgluco
25	38	48.7	422	2 T21820	hypothetical prote
26	38	48.7	553	2 I37417	glycerol kinase -
27	38	48.7	781	2 C69452	signal-transducing
28	38	48.7	876	2 T19246	hypothetical prote
29	38	48.7	1403	2 S24548	homeotic protein p

30	37	47.4	219	2 T47881	hypothetical prote
31	37	47.4	220	2 E90022	50S ribosomal prot
32	37	47.4	253	2 H90891	probable ARAC-type
33	37	47.4	253	2 A85726	probable ARAC-type
34	37	47.4	253	2 P64903	transcription regu
35	37	47.4	296	2 AC0231	probable binding-p
36	37	47.4	296	2 T47062	hypothetical prote
37	37	47.4	339	2 H86210	hypothetical prote
38	37	47.4	341	2 I61725	natural killer ase
39	37	47.4	347	2 T06671	hypothetical prote
40	37	47.4	348	2 A56247	natural killer cel
41	37	47.4	427	2 G02034	killer cell inhibi
42	37	47.4	444	2 G01924	KIR (Cl-2) NK rece
43	37	47.4	444	2 G01925	KIR (Cl-11) NK rece
44	37	47.4	455	2 G01923	KIR (Cl-5) NK rece
45	37	47.4	497	2 T29791	hypothetical prote

ALIGNMENTS

RESULT 1

JH0557
exo-alpha-sialidase (EC 3.2.1.18) - Trypanosoma cruzi
N;Alternate names: neuraminidase
C;Species: Trypanosoma cruzi
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JH0557
R;Pereira, M.E.A.; Mejia, J.S.; Ortega-Barria, E.; Matzilevich, D.; Prioli, R.P.
J. Exp. Med. 174, 179-191, 1991
A;Title: The Trypanosoma cruzi neuraminidase contains sequences similar to bacterial ne
A;Reference number: JH0557; MUID:91277609, PMID:1711561
A;Accession: JH0557
A;Molecule type: DNA
A;Residues: 1-1162 <PER>
A;Cross-references: UNIPROT:P23253; GB:M61732; NID:G162302; PID:G162303
A;Note: the authors translated the codon TCT for residue 45 as Cys
C;Comment: This protein plays a role in parasite-host cell interaction.
C;Superfamily: trypanastigote-specific surface antigen
C;Keywords: glycoprotein; glycosidase; hydrolase
F;394/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 78; DB 2; Length 1162;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQRLPKRMGGSYRC 14

Db 379 RQRLPKRMGGSYRC 392

RESULT 2

AE1851
hypothetical protein asr0358 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE1851
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE1851
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <KUR>
A;Cross-references: UNIPROT:Q8YZU7; GB:BA000019; PIDN:BA072316.1; PID:G17129703; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asr0358

Query Match 52.6%; Score 41; DB 2; Length 83;

Best Local Similarity 38.5%; Pred. No. 5.8;
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 QRLPKRMGGSYRC 14
Db 46 RNIAKJLGGNFR 58

RESULT 3
H75403
glycosyl hydrolase, family 13 - Deinococcus radiodurans (strain R1)
C/Species: Deinococcus radiodurans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: H75403
R/White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A/Reference number: A75250; MUID:20036896; PMID:10567266
A/Accession: H75403
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-564 <WHI>
A/Cross-references: UNIPROT:Q9RUK9; GB:AE001983; GB:AE000513; NID:G6459123; PIDN:AAF1094
A/Experimental source: strain R1
C/Genetics:
A/Gene: DR1375
A/Map position: 1.
C/Superfamily: alpha-glucosidase; alpha-amylase core homology

Query Match 52.6%; Score 41; DB 2; Length 564;
Best Local Similarity 61.5%; Pred. No. 34;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RQRLPKRMGGSYR 13
Db 487 RQEQPALVGGSYR 499

RESULT 4
JU0029
tumor necrosis factor alpha precursor - rat
N/Alternate names: cachectin; TNF alpha
C/Species: Rattus norvegicus (Norway rat)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C/Accession: JU0029; JN0868; S21674
R/Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
Agric. Biol. Chem. 53, 1733-1736, 1989
A/Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis f
A/Reference number: JU0029
A/Accession: JU0029
A/Molecule type: DNA
A/Residues: 1-235 <SHI>
A/Cross-references: UNIPROT:P16599
R/Kwon, J.; Chung, I.Y.; Benveniste, E.N.
Gene 132, 227-236, 1993
A/Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
A/Reference number: JN0868; MUID:94040766; PMID:8224868
A/Accession: JN0868
A/Molecule type: DNA
A/Residues: 1-235 <KWO>
A/Cross-references: GB:L00981; NID:G205253; PIDN:AAA16275.1; PID:G205254
R/Estler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.
Biol. Chem. Hoppe-Seyler 373, 271-281, 1992
A/Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitr
A/Reference number: S21674; MUID:92329007; PMID:1627266
A/Accession: S21674
A/Molecule type: mRNA
A/Residues: 1-38, 'P', 40-162, 'T', 164-201, 'S', 203-235 <EST>
A/Cross-references: GB:X66539; GB:S40199; NID:G395369; PIDN:CAA47146.1; PID:G395370
C/Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and
C/Genetics:

A/Gene: TNF-alpha
A/Introns: 62/3; 81/1; 97/1
C/Superfamily: tumor necrosis factor
C/Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memt
F/80-235/Product: tumor necrosis factor #status predicted <MAT>
F/19,20/Binding site: myristate (Lys) (covalent) #status predicted
F/84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F/86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/148-179/Disulfide bonds: #status predicted

Query Match 51.9%; Score 40.5; DB 2; Length 235;
Best Local Similarity 56.2%; Pred. No. 18;
Matches 9; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 2 QRLPKRMGG--SYRC 14
Db 15 EALPKRMGGGLQNSRR 30

RESULT 5
G65067
hypothetical protein b2846 - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C/Accession: G65067
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: G65067
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-230 <BLAT>
A/Cross-references: GB:AE000368; GB:U00096; NID:G2367165; PIDN:AAC75885.1; PID:G1789212;
A/Experimental source: strain K-12, substrain MGL655

Query Match 51.3%; Score 40; DB 2; Length 230;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RQRLPKRMGG 10
Db 207 KQRIEKRMMGG 216

RESULT 6
B85937
hypothetical protein yqeH [imported] - Escherichia coli (strain O157:H7, substrain EDL9;
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: B85937
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhev
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: B85937
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-230 <STO>
A/Cross-references: UNIPROT:Q8X6I5; GB:AE005174; NID:G12517338; PIDN:AAG57958.1; GSPDB:(
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: yqeH

Query Match 51.3%; Score 40; DB 2; Length 230;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RQRLPKRMGG 10
Db 207 KQRIEKRMMGG 216

RESULT 7

G91091
hypothetical protein ECs3703 [imported] - Escherichia coli (strain O157:H7, substrain R1)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: G91091
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G91091
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-230 <HAY>
A;Cross-references: UNIPROT:Q8X6I5; GB:BA000007; PIDN:BA037126.1; PID:G13363175; GSPDB:G13363175
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: ECs3703

Query Match 51.3%; Score 40; DB 2; Length 230;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RQRLPKRMGG 10
:|:|:|:|
Db 207 KQRIEKRMG 216

RESULT 8

JQ0137
hypothetical 30.1k protein - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Jun-1996
C;Accession: JQ0137
R;Kato, J.; Chu, L.; Kitano, K.; Devault, J.D.; Kimbara, K.; Chakrabarty, A.M.; Misra, T.
Gene 84, 31-38, 1989
A;Title: Nucleotide sequence of a regulatory region controlling alginate synthesis in Pseudomonas aeruginosa
A;Reference number: JQ0137; MUID:90108714; PMID:2514124
A;Accession: JQ0137
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-261 <KAT>
A;Note: 3-Met could also be the initiator
C;Genetics:
A;Start codon: GTG

Query Match 51.3%; Score 40; DB 2; Length 261;
Best Local Similarity 57.1%; Pred. No. 25;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RQRLPKRMGGSYRC 14
:|:|:|:|
Db 31 RQRLRRWSGRRRC 44

RESULT 9

F75504
probable pilin, type IV - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: F75504
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F75504
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-314 <WHI>
A;Cross-references: UNIPROT:Q9RW7; GB:AE001913; GB:AE000513; NID:G6458240; PIDN:AAF101
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0548
A;Map position: 1

Query Match 51.3%; Score 40; DB 2; Length 314;
Best Local Similarity 72.7%; Pred. No. 30;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQRLPKRMGG 11
:|:|:|:|
Db 26 RQRPQRQGG 36

RESULT 10

H86890
hypothetical protein yvjB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86890
R;Bolotin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86890
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-428 <STO>
A;Cross-references: UNIPROT:Q9CDT3; GB:AE005176; PID:G12725185; PIDN:AAK06226.1; GSPDB:
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yvjB

Query Match 51.3%; Score 40; DB 2; Length 428;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PKRMGGSYR 13
:|:|:|:|
Db 280 PKRMGGSYR 288

RESULT 11

T51756
NAD+ synthase (glutamine-hydrolyzing) (EC 6.3.5.1) [imported] - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51756
R;Fink, D.; Falke, D.; Wohlleben, W.; Engels, A.
Microbiology 145, 2313-2322, 1999
A;Title: Nitrogen metabolism in Streptomyces coelicolor A3(2): modification of glutamin
A;Reference number: Z25448
A;Accession: T51756
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-538 <FIN>
A;Cross-references: UNIPROT:Q9Z4V9; EMBL:Y17736; PIDN:CAB38325.1
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: nadE
C;Superfamily: Rhodobacter capsulatus NH3-dependent NAD+ synthase
C;Keywords: ligase

Query Match 51.3%; Score 40; DB 2; Length 538;
Best Local Similarity 70.0%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PKRMGGSYRC 14
:|:|:|:|
Db 233 PGRLLGGSSRC 242

RESULT 12

T07757

probable DNA (cytosine-5-)-methyltransferase (EC 2.1.1.37) - tomato

C/Species: Lycopersicon esculentum (tomato)

C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004

C/Accession: T07757

R/Cella, R.

submitted to the EMBL Data Library, October 1997

A/Reference number: Z16119

A/Accession: T07757

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1559 <CEL>

A/Cross-references: UNIPROT:O49889; EMBL:AJ002140; NID:e1250983; PIDN:CAA05207.1; PID:e1

A/Experimental source: cultivar Meraviglia; apical meristems

C/Genetics:

A/Gene: sMET

C/Keywords: methyltransferase; S-adenosylmethionine

Query Match 51.3%; Score 40; DB 2; Length 1559;

Best Local Similarity 58.3%; Pred. No. 1.3e+02;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 QRLPKRMGGSYR 13

Db 1423 QRIPKRPQADWR 1434

RESULT 13

B71013

hypothetical protein PH1400 - Pyrococcus horikoshii

C/Species: Pyrococcus horikoshii

C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004

C/Accession: B71013

R/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A/Reference number: A71000; MUID:98344137; PMID:9679194

A/Accession: B71013

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-298 <KAW>

A/Cross-references: UNIPROT:O50108; GB:AP000006; NID:G3236133; PIDN:BAA30506.1; PID:d103

A/Experimental source: strain OT3

A/Note: this accession replaces an interim accession for a sequence replaced by GenBank

C/Genetics:

A/Gene: PH1400

Query Match

Best Local Similarity 50.0%; Score 39; DB 2; Length 298;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 RLPKRMGGSYR 13

Db 51 RLKKRLGGIYK 61

RESULT 14

G81395

probable ATP /GTP binding protein Cj0500 [imported] - Campylobacter jejuni (strain NCTC

C/Species: Campylobacter jejuni

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C/Accession: G81395

R/Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillir

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel

Nature 403, 665-668, 2000

A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A/Reference number: A81250; MUID:20150912; PMID:10688204

A/Accession: G81395

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-332 <PAR>

A/Cross-references: UNIPROT:Q9PI09; GB:AL139075; GB:AL111168; NID:G6967817; PIDN:CAB751;

A/Experimental source: serotype O2, strain NCTC 11168

C/Genetics:

A/Gene: Cj0500

Query Match

Best Local Similarity 50.0%; Score 39; DB 2; Length 332;

Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 QRLPKRMGGSYR 14

Db 57 QALAKAMGASYIC 69

RESULT 15

C90498

carnitine dehydratase, probable [imported] - Sulfolobus solfataricus

C/Species: Sulfolobus solfataricus

C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C/Accession: C90498

R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, I

arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A/Description: Sulfolobus solfataricus complete genome.

A/Reference number: A99139

A/Accession: C90498

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-372 <KUR>

A/Cross-references: UNIPROT:Q97U79; GB:AE006641; NID:G13816568; PIDN:AAK43242.1; GSPDB:(

C/Genetics:

A/Gene: SSO3144

C/Supfamily: Mycobacterium tuberculosis hypothetical protein Rv3272

Query Match

Best Local Similarity 50.0%; Score 39; DB 2; Length 372;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 RLPKRMGGSYR 13

Db 209 KVPKRMGSAHR 219

Search completed: November 18, 2005, 00:29:46

Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 22:29:58 ; Search time 79 Seconds
(without alignments)
90.748 Million cell updates/sec

Title: US-09-745-008-14
Perfect score: 78
Sequence: 1 RQRLPKRMGGSYRC 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	100.0	1162	1 TCNA_TRYCR	P23253 trypanosoma
2	47	60.3	487	2 Q6LG50	Q61g50 photobacter
3	47	60.3	487	2 Q7MBZ4	Q7mbz4 vibrio vuln
4	47	60.3	487	2 Q8D557	Q8d557 vibrio vuln
5	47	60.3	488	2 Q87FH4	Q87fh4 vibrio para
6	44	56.4	244	2 Q8JKU8	Q8jku8 heliothis z
7	44	56.4	823	2 Q7PSQ4	Q7psq4 anopheles g
8	43	55.1	224	2 Q6ZON4	Q6zon4 oryza sativ
9	42	53.8	107	2 Q68807	Q68807 synecococc
10	42	53.8	339	2 Q9VUB3	Q9vub3 drosophila
11	42	53.8	474	2 Q89Y78	Q89y78 bradyrhizob
12	42	53.8	722	2 Q6GNB3	Q6gnb3 xenopus lae
13	42	53.8	1169	1 IF2_PROMP	Q7uzz9 prochloroco
14	41	52.6	83	2 Q8YZU7	Q8yzu7 anabaena sp
15	41	52.6	384	2 Q7UES8	Q7ues8 rhodopirell
16	41	52.6	564	2 Q9RUK9	Q9ruk9 deinococcus
17	41	52.6	694	2 Q63JI7	Q63ji7 burkholderi
18	41	52.6	1065	2 Q6MG21	Q6mg21 rattus norv
19	40.5	51.9	235	1 TNFA_RAT	P16599 rattus norv
20	40.5	51.9	748	2 Q8LQH6	Q8lqh6 oryza sativ
21	40	51.3	150	2 Q82JH6	Q82jh6 streptomyce
22	40	51.3	151	2 Q9K4D3	Q9k4d3 streptomyce
23	40	51.3	181	2 Q6H705	Q6h705 oryza sativ
24	40	51.3	210	1 YQEH_ECOLI	Q46941 escherichia
25	40	51.3	230	2 Q8X6I5	Q8x6i5 escherichia
26	40	51.3	314	2 Q9RWV7	Q9rwv7 deinococcus
27	40	51.3	384	2 Q657J9	Q657j9 oryza sativ
28	40	51.3	428	1 YL28_LACLA	Q9cdt3 lactococcus
29	40	51.3	507	2 Q8KW84	Q8kw84 ruegeria sp
30	40	51.3	533	2 Q6ZIE6	Q6zie6 oryza sativ
31	40	51.3	538	2 Q9Z4V9	Q9z4v9 streptomyce

32	40	51.3	559	2 Q969Y0	Q969y0 homo sapien
33	40	51.3	885	2 Q8HYV1	Q8hyv1 sus scrofa
34	40	51.3	886	2 Q8HYV2	Q8hyv2 sus scrofa
35	40	51.3	955	1 MDG1_HUMAN	Q8nfp4 homo sapien
36	40	51.3	1556	2 Q9MB97	Q9mb97 nicotiana t
37	40	51.3	1559	2 Q49889	Q49889 lycopersico
38	40	51.3	1955	2 Q8W078	Q8w078 oryza sativ
39	39.5	50.6	619	2 Q8BWQ5	Q8bwq5 mus musculu
40	39	50.0	61	2 Q83177	Q83177 cauliflower
41	39	50.0	203	2 Q8N9P6	Q8n9p6 homo sapien
42	39	50.0	277	2 Q7X801	Q7x801 oryza sativ
43	39	50.0	298	2 Q50108	Q50108 pyrococcus
44	39	50.0	304	1 K2S3_HUMAN	Q14952 homo sapien
45	39	50.0	311	1 STCC_EMENI	Q00668 emericella

ALIGNMENTS

RESULT 1
TCNA_TRYCR STANDARD; PRT; 1162 AA.
AC P23253;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Sialidase (EC 3.2.1.18) (Neuraminidase) (NA) (Major surface antigen).
GN Name=TCNA;
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Silvio X-10/4;
RX MEDLINE=91277609; PubMed=1711561;
RA Pereira M.E.A., Mejia J.S., Ortega-Barria E., Matzilevich D., Prioli R.P.;
RA "The Trypanosoma cruzi neuraminidase contains sequences similar to bacterial neuraminidases, YWTD repeats of the low density lipoprotein receptor, and type III modules of fibronectin.";
RL J. Exp. Med. 174:179-191(1991).
RN [2]
SUBCELLULAR LOCATION.
MEDLINE=91376547; PubMed=1896773;
PRIOLI R.P., Mejia J.S., Aji T., Aikawa M., Pereira M.E.A.;
"Trypanosoma cruzi: localization of neuraminidase on the surface of trypanastigotes.";
Trop. Med. Parasitol. 42:146-150(1991).
CC -|- FUNCTION: Developmentally regulated neuraminidase implicated in parasite invasion of cells.
CC -|- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
CC -|- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (Potential).
CC -|- DEVELOPMENTAL STAGE: Maximal activity in trypomastigotes, minimum in epimastigotes and not detectable in amastigotes.
CC -|- MISCELLANEOUS: The variable lengths of the long tandem repeat domain could account in part for the polymorphism of the TCNA protein.
CC -|- SIMILARITY: Belongs to the glycosyl hydrolase 33 family.
CC -|- SIMILARITY: Contains 3 BNR repeats.

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EMBL; M61732; AAA30255.1; -.

DR PIR; JH0557; JH0557.
DR HSSP; Q26966; 1MR5.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR002860; Glyco_hydro_BNR.
DR InterPro; IPR011040; Sialidase.
DR InterPro; IPR008377; Sialidase_trypan.
DR Pfam; PF02012; BNR; 2.
DR PRINTS; PR01803; TCSIALIDASE.
KW Glycoprotein; Glycosidase; GPI-anchor; Hydrolase; Phosphorylation;
KW Repeat.
FT DOMAIN 1 457 Cys-rich.
FT REPEAT 23 34 BNR 1.
FT REPEAT 163 174 BNR 2.
FT REPEAT 209 220 BNR 3.
FT DOMAIN 458 588 Fibronectin type-III.
FT DOMAIN 589 1120 44 X 12 AA tandem repeats, LTR domain.
FT CARBOHYD 342 342 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 394 394 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1125 1125 N-linked (GlcNAc. . .) (Potential).
SQ SEQUENCE 1162 AA; 120032 MW; 07049221897C6A40 CRC64;

Query Match 100.0%; Score 78; DB 1; Length 1162;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQLPKRMGGSYRC 14
Db |||||
379 RQLPKRMGGSYRC 392

RESULT 2
Q6LG50 PRELIMINARY; PRT; 487 AA.
AC Q6LG50;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative mannose oxidoreductase.
GN Name=Y2903; OrderedLocusNames=PBPRB1880;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR378680; CAG23730.1; -.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008927; 6GDH C like.
DR InterPro; IPR000669; Mannitol_dh.
DR Pfam; PF01232; Mannitol dh; 1.
DR PRINTS; PR00084; MTLDDHGRGNASE.
DR PROSITE; PS00974; MANNITOL_DHGENASE; 1.
KW Complete proteome.
SQ SEQUENCE 487 AA; 53733 MW; 35525999038BB279 CRC64;

Query Match 60.3%; Score 47; DB 2; Length 487;
Best Local Similarity 66.7%; Pred. No. 7.3;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRLPKRMGGSYR 13
Db |:::|||||
376 QKIPQRMGGSLR 387

RESULT 3
Q7MB24 PRELIMINARY; PRT; 487 AA.
AC Q7MB24;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mannonate oxidoreductase.
GN OrderedLocusNames=VVA1593;
OS Vibrio vulnificus (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C., Tsai H.-C., Su T.-L.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587(2003).
DR EMBL; AP005350; BAC97619.1; -.
DR HSSP; O08355; 1LJ8.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008927; 6GDH C like.
DR InterPro; IPR000669; Mannitol_dh.
DR Pfam; PF01232; Mannitol dh; 1.
DR PRINTS; PR00084; MTLDDHGRGNASE.
DR PROSITE; PS00974; MANNITOL_DHGENASE; 1.
KW Complete proteome.
SQ SEQUENCE 487 AA; 53290 MW; 570C961191EB96CE CRC64;

Query Match 60.3%; Score 47; DB 2; Length 487;
Best Local Similarity 66.7%; Pred. No. 7.3;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRLPKRMGGSYR 13
Db |:::|||||
376 QKIPQRMGGSLR 387

RESULT 4
Q8D557 PRELIMINARY; PRT; 487 AA.
AC Q8D557;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mannitol-1-phosphate/altronate dehydrogenase.
GN OrderedLocusNames=VV21069;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016811; AA007976.1; -.
DR HSSP; O08355; 1LJ8.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008927; 6GDH C like.
DR InterPro; IPR000669; Mannitol_dh.
DR Pfam; PF01232; Mannitol dh; 1.
DR PRINTS; PR00084; MTLDDHGRGNASE.
DR PROSITE; PS00974; MANNITOL_DHGENASE; 1.
KW Complete proteome.
SQ SEQUENCE 487 AA; 53408 MW; 28786B2A15172F7D CRC64;

Query Match 60.3%; Score 47; DB 2; Length 487;
Best Local Similarity 66.7%; Pred. No. 7.3;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRLPKRMGGSYR 13
|:|:|:|:|:|:|
Db 376 QKIPQRMGGSLR 387

RESULT 5

ID Q87FH4 PRELIMINARY; PRT; 488 AA.
AC Q87FH4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mannonate oxidoreductase.
GN OrderedLocusNames=VPA1705;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najiima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; AP005089; BAC63048.1; -.
DR HSSP; O08355; 1LJ8.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008927; 6GDGH C like.
DR InterPro; IPR000669; Mannitol_dh.
DR Pfam; PF01232; Mannitol dh; 1.
DR PRINTS; PR00084; MTLHDHGRNASE.
DR PROSITE; PS00974; MANNITOL_DHCENASE; 1.
KW Complete proteome.
SQ SEQUENCE 488 AA; 53509 MW; 700EED77E6BD56F4 CRC64;

Query Match 60.3%; Score 47; DB 2; Length 488;
Best Local Similarity 66.7%; Pred. No. 7.4;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRLPKRMGGSYR 13
|:|:|:|:|:|:|
Db 376 QKIPQRMGGSLR 387

RESULT 6

ID Q8JKUB PRELIMINARY; PRT; 244 AA.
AC Q8JKUB;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Orf13.
GN Names=Orf13;
OS Heliothis zea virus 1.
OC Viruses; dsDNA viruses, no RNA stage; unclassified dsDNA viruses.
OX NCBI_TaxID=29250;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22174892; PubMed=12186886;
RX DOI=10.1128/JVI.76.18.9024-9034.2002;
RA Cheng C.H., Liu S.M., Chow T.Y., Hsiao Y.Y., Wang D.P., Huang J.J.,
RA Chen H.H.;
RT "Analysis of the complete genome sequence of the Hz-1 virus suggests
that it is related to members of the Baculoviridae.";

RL J. Virol. 76:9024-9034(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Cheng C.H., Liu H.M., Hsiao Y.Y., Chow T.Y., Chen H.H.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Chao Y.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBSJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Chen H.H., Yeh W.B., Tso D.J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBSJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Cheng C.H., Hsiao Y.Y., Liu S.M., Chow T.Y., Chen H.H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF451898; AAN04308.1; -.
SQ SEQUENCE 244 AA; 28641 MW; 3DA50433BE14D855 CRC64;

Query Match 56.4%; Score 44; DB 2; Length 244;
Best Local Similarity 53.8%; Pred. No. 13;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQRLPKRMGGSYR 13
|:|:|:|:|:|:|
Db 14 KERTPKRLEGTYR 26

RESULT 7

ID Q7PSQ4 PRELIMINARY; PRT; 823 AA.
AC Q7PSQ4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000017954 (Fragment).
GN Name=ENSANGG00000015465;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBSJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB0100816; EAA05197.2; -.
DR HSSP; P35555; 1EMN.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07645; EGF_CA; 11.
DR PROSITE; PS00010; ASX HYDROXYL; 5.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS50026; EGF_3; 4.
DR PROSITE; PS01187; EGF_CA; 10.
KW EGF-like domain.
FT NON TER 1
SQ SEQUENCE 823 AA; 90711 MW; 8B9CDA78DD291E1F CRC64;

Query Match 56.4%; Score 44; DB 2; Length 823;
Best Local Similarity 57.1%; Pred. No. 45;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RQRLPKRMGGSYR 14
|:|:|:|:|:|:|

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Db 714 RQDICTNIGGSYRC 727

RESULT 8
Q6ZON4
ID Q6ZON4 PRELIMINARY; PRT; 224 AA.
AC Q6ZON4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein OJ1212_C09.7.
GN Name=OJ1212_C09.7;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005487; BAD01415.1; -.
DR InterPro; IPR007087; Znf_C2H2.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 224 AA; 24522 MW; 92ED74475991235B CRC64;

Query Match 55.1%; Score 43; DB 2; Length 224;
Best Local Similarity 64.3%; Pred. No. 18;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 3 RLPK--RMGGSYRC 14
|||: |||||
DB 109 RLPRVSRSGPYRC 122

RESULT 9
Q68807
ID Q68807 PRELIMINARY; PRT; 107 AA.
AC Q68807;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32049;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC7002;
RA Droog F.N.J., Taller B.J., Stevens S.E. Jr.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF054515; AAC08034.1; -.
KW Hypothetical protein.
FT NON TER 107
SQ SEQUENCE 107 AA; 12163 MW; A5A44929EB610569 CRC64;

Query Match 53.8%; Score 42; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QRLPKRMGGSYR 13
|||: |||
DB 36 QRLAKRLGAHYR 47

RESULT 10
Q9VUB3
ID Q9VUB3 PRELIMINARY; PRT; 339 AA.
AC Q9VUB3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)

```

RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleeb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003536; AAF49775.1; -;
DR EMBL; AY071545; AAL49167.1; -;
DR HSSP; P08045; 1ZNP.
DR IntAct; Q9VUB3; -;
DR FlyBase; FBgn0036396; CG17359.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR007087; Znf C2H2.
DR Pfam; PF00096; zf-C2H2; 4.
DR SMART; SM00355; Znf C2H2; 5.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
SQ SEQUENCE 339 AA; 39250 MW; 9B653D457205C57A CRC64;

Query Match 53.8%; Score 42; DB 2; Length 339;
Best Local Similarity 70.0%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PKRMGGSYRC 14
|||: |||
DB 208 PKRVPGPYRC 217

RESULT 11
Q89Y78 PRELIMINARY; PRT; 474 AA.
AC Q89Y78;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Blr0077 protein.
GN OrderedLocusNames=blr0077;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium

RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005935; BAC45342.1; -;
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0009116; P:nucleoside metabolism; IEA.
DR InterPro; IPR003615; HNH_nuc.
DR InterPro; IPR000845; PNP_UDP.
DR Pfam; PF01048; PNP_UDP_1; 1.
DR SMART; SM00507; HNHc; 1.
KW Complete proteome.
SQ SEQUENCE 474 AA; 52343 MW; 9537C1AE90B07BB4 CRC64;

Query Match 53.8%; Score 42; DB 2; Length 474;
Best Local Similarity 61.5%; Pred. No. 59;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RQRLPKRMGGSYR 13
|: |||
DB 169 RGTIPTRGGSYR 181

RESULT 12
Q6GNB3 PRELIMINARY; PRT; 722 AA.
AC Q6GNB3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC82906 protein.
GN Name=MGC82906;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BC073602; AAH73602.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 5.
DR SMART; SM00409; IG; 6.
DR SMART; SM00408; IGC2; 4.
DR PROSITE; PS50835; IG_LIKE; 5.
SQ SEQUENCE 722 AA; 78786 MW; ABAF5411CA28EF87 CRC64;

Query Match 53.8%; Score 42; DB 2; Length 722;
Best Local Similarity 46.2%; Pred. No. 92;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 QRLPKRMGGSYRC 14
:|:|:|:|:|
Db 351 ERVPEDYGGGYQC 363

RESULT 13
IF2 PROMP STANDARD; PRT; 1169 AA.
AC Q7UZZ9;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Translation initiation factor IF-2.
GN Name=infB; OrderedLocusNames=PMW1494;
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=59919;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
CC -!- FUNCTION: One of the essential components for the initiation of
CC protein synthesis. Protects formylmethionyl-tRNA from spontaneous
CC hydrolysis and promotes its binding to the 30S ribosomal subunits.
CC Also involved in the hydrolysis of GTP during the formation of the
CC 70S ribosomal complex (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the IF-2 family.
CC
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; BX572094; CAE19953.1; -.
DR HAMAP; MF 00100; -; 1.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR000178; IF2.
DR InterPro; IPR006847; IF2_N.
DR InterPro; IPR000795; ProtSyn_GTPbind.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR Pfam; PF04760; IF2_N; 2.
DR ProDom; PD186100; IF2; 1.
DR TIGRFAMs; TIGR00487; IF-2; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR PROSITE; PS01176; IF2; 1.
```

```
KW Complete proteome; GTP-binding; Initiation factor;
KW Protein biosynthesis.
FT DOMAIN 664 816 G-domain.
FT NP_BIND 670 677 GTP (By similarity).
FT NP_BIND 720 724 GTP (By similarity).
FT NP_BIND 774 777 GTP (By similarity).
SQ SEQUENCE 1169 AA; 127147 MW; 0705D909F5377562 CRC64;

Query Match 53.8%; Score 42; DB 1; Length 1169;
Best Local Similarity 61.5%; Pred. No. 1.5e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QRLPKRMGGSYR 13
:|:|:|:|:|
Db 292 RQGVNREGGYPYR 304

RESULT 14
Q8YZU7 PRELIMINARY; PRT; 83 AA.
AC Q8YZU7;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Asr0358 protein.
GN OrderedLocusNames=asr0358;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003582; BAB72316.1; -.
DR PIR; AE1851; AE1851.
DR GO; GO:0005524; F:ATP binding; IEA.
DR Pfam; PF02518; HATPase_C; 1.
KW Complete proteome.
SQ SEQUENCE 83 AA; 9321 MW; B315C9D52BD404EC CRC64;

Query Match 52.6%; Score 41; DB 2; Length 83;
Best Local Similarity 38.5%; Pred. No. 15;
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
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QY 2 QRLPKRMGGSYRC 14
:|:|:|:|:|
Db 46 RNIAKXKLGNGFRC 58

RESULT 15
Q7UES8 PRELIMINARY; PRT; 384 AA.
AC Q7UES8;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RB10581;
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
```


RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.,
RT "Complete genome sequence of the marine planctomycete *Pirellula* sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
DR EMBL; BX294151; CAD78956.1; -.
DR InterPro; IPR011453; DUF1559.
DR InterPro; IPR001120; Prok_N_methyl_S.
DR Pfam; PF07596; SBP_bac_10; 1.
DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
KW Complete proteome; Hypothetical protein; Methylation.
SQ SEQUENCE 384 AA; 41431 MW; 4D737552773F70F4 CRC64;

Query Match 52.6%; Score 41; DB 2; Length 384;
Best Local Similarity 50.0%; Pred. No. 73;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 3 RLPKRMGGSYRC 14
:|::|||:|
Db 68 QFPQMGGRYCC 79

Search completed: November 18, 2005, 00:29:20
Job time : 87 secs

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OM protein - protein search, using sw model

Run on: November 18, 2005, 00:23:59 ; Search time 26 Seconds
(without alignments)
40.196 Million cell updates/sec

Title: US-09-745-008-14

Perfect score: 78

Sequence: 1 RQRLPKRMGGSYRC 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	57.7	433	US-09-252-991A-28695	Sequence 28695, A
2	43	55.1	164	US-09-252-991A-20615	Sequence 20615, A
3	43	55.1	164	US-09-252-991A-30154	Sequence 30154, A
4	43	55.1	223	US-09-252-991A-18819	Sequence 18819, A
5	43	55.1	545	US-09-252-991A-30417	Sequence 30417, A
6	42.5	54.5	1107	US-09-489-039A-8890	Sequence 8890, Ap
7	42	53.8	30	US-09-205-258-1167	Sequence 1167, Ap
8	42	53.8	419	US-09-252-991A-17499	Sequence 17499, A
9	41.5	53.2	381	US-09-902-540-11854	Sequence 11854, A
10	41	52.6	492	US-09-252-991A-20531	Sequence 20531, A
11	41	52.6	511	US-09-252-991A-18691	Sequence 18691, A
12	41	52.6	556	US-09-252-991A-22588	Sequence 22588, A
13	41	52.6	595	US-09-252-991A-17469	Sequence 17469, A
14	40	51.3	303	US-09-252-991A-22757	Sequence 22757, A
15	40	51.3	355	US-09-252-991A-27426	Sequence 27426, A
16	40	51.3	362	US-09-252-991A-30626	Sequence 30626, A
17	40	51.3	419	US-09-252-991A-28487	Sequence 28487, A
18	40	51.3	422	US-09-252-991A-18660	Sequence 18660, A
19	40	51.3	518	US-09-252-991A-25967	Sequence 25967, A
20	40	51.3	939	US-09-540-236-2399	Sequence 2399, Ap
21	39	50.0	232	US-09-489-039A-10126	Sequence 10126, A
22	39	50.0	542	US-08-412-431-3	Sequence 3, Appli
23	39	50.0	542	US-08-623-679-3	Sequence 3, Appli
24	39	50.0	542	US-08-933-774-3	Sequence 3, Appli
25	39	50.0	542	US-09-181-030-3	Sequence 3, Appli
26	39	50.0	542	US-09-534-242-3	Sequence 3, Appli
27	39	50.0	542	US-09-454-854-3	Sequence 3, Appli

28	39	50.0	542	3	US-09-164-671-3	Sequence 3, Appli
29	39	50.0	542	4	US-09-182-113-3	Sequence 3, Appli
30	39	50.0	542	4	US-08-862-442-3	Sequence 3, Appli
31	39	50.0	1319	4	US-09-538-092-1291	Sequence 1291, Ap
32	39	50.0	1343	4	US-09-949-016-10641	Sequence 10641, A
33	39	50.0	1497	1	US-08-623-679-7	Sequence 7, Appli
34	39	50.0	1497	3	US-08-933-774-7	Sequence 7, Appli
35	39	50.0	1497	3	US-09-181-030-7	Sequence 7, Appli
36	39	50.0	1497	3	US-09-534-242-7	Sequence 7, Appli
37	39	50.0	1497	3	US-09-454-854-7	Sequence 7, Appli
38	39	50.0	1497	3	US-09-164-671-7	Sequence 7, Appli
39	39	50.0	1497	4	US-09-182-113-7	Sequence 7, Appli
40	39	50.0	1497	4	US-08-862-442-7	Sequence 7, Appli
41	39	50.0	1533	1	US-08-623-679-9	Sequence 9, Appli
42	39	50.0	1533	3	US-08-933-774-9	Sequence 9, Appli
43	39	50.0	1533	3	US-09-181-030-9	Sequence 9, Appli
44	39	50.0	1533	3	US-09-534-242-9	Sequence 9, Appli
45	39	50.0	1533	3	US-09-454-854-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-252-991A-28695
; Sequence 28695, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28695
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28695

Query Match 57.7%; Score 45; DB 4; Length 433;
Best Local Similarity 64.3%; Pred. No. 5.8;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RQRLPKRMGGSYRC 14
|:|:|:|:|:|:|:|:|:|
Db 251 RRRLPVRPGGPGRC 264

RESULT 2
US-09-252-991A-20615
; Sequence 20615, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20615
; LENGTH: 164
; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20615

Query Match 55.1%; Score 43; DB 4; Length 164;
Best Local Similarity 50.0%; Pred. No. 4.7;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RQRLPKRMGGSYRC 14
|:|:|:|:|:|:|:
Db 73 RRRMPRRSGPATRC 86

RESULT 3

US-09-252-991A-30154
; Sequence 30154, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 30154

; LENGTH: 164

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-30154

Query Match 55.1%; Score 43; DB 4; Length 164;
Best Local Similarity 50.0%; Pred. No. 4.7;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RQRLPKRMGGSYRC 14
|:|:|:|:|:|:|:
Db 73 RRRMPRRSGPATRC 86

RESULT 4

US-09-252-991A-18819
; Sequence 18819, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 18819

; LENGTH: 223

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-18819

Query Match 55.1%; Score 43; DB 4; Length 223;
Best Local Similarity 58.3%; Pred. No. 6.5;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RQRLPKRMGGSY 12
|:|:|:|:|:|:|:
Db 183 RQRIPIRRRGGRH 194

RESULT 5

US-09-252-991A-30417
; Sequence 30417, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 30417

; LENGTH: 545

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-30417

Query Match 55.1%; Score 43; DB 4; Length 545;
Best Local Similarity 61.5%; Pred. No. 17;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RQRLPKRMGGSYR 13
|:|:|:|:|:|:|:
Db 56 RSRLPRRAGGEVR 68

RESULT 6

US-09-489-039A-8890
; Sequence 8890, Application US/09489039A
; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 8890

; LENGTH: 1107

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-8890

Query Match 54.5%; Score 42.5; DB 4; Length 1107;
Best Local Similarity 64.3%; Pred. No. 45;
Matches 9; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 RQR-LPKRMGGSYR 13
|:|:|:|:|:|:|:
Db 19 RQRPVPDRLGQYR 32

RESULT 7

US-09-205-258-1167
; Sequence 1167, Application US/09205258
; Patent No. 6525174

; GENERAL INFORMATION:

; APPLICANT: Young et al.

; TITLE OF INVENTION: 207 Human Secreted Proteins

; FILE REFERENCE: P2007P1

; CURRENT APPLICATION NUMBER: US/09/205,258

; CURRENT FILING DATE: 1998-12-04

; EARLIER APPLICATION NUMBER: PCT/US98/11422

; EARLIER FILING DATE: 1998-06-04

; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923

; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1167
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-1167

Query Match 53.8%; Score 42; DB 4; Length 30;
Best Local Similarity 61.5%; Pred. No. 1.1;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RQRLPKRMGGSYR 13
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Db 5 RQRRPRRRGGTSR 17

RESULT 8
US-09-252-991A-17499
; Sequence 17499, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17499
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17499

Query Match 53.8%; Score 42; DB 4; Length 419;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PKRMGGSYRC 14
| | | | | | | | | |
Db 359 PRRSGGEFRC 368

RESULT 9
US-09-902-540-11854
; Sequence 11854, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11854
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Myxococcus xanthus

US-09-902-540-11854

Query Match	53.2%	Score 41.5;	DB 4;	Length 381;
Best Local Similarity	50.0%	Pred. No. 22;		
Matches 10;	Conservative	2;	Mismatches 1;	Indels 7;
			Gaps	1;

Qy 1 RQRLPKRMGG-----SYR 13
|:|:|:|:|
Db 113 RKSLPQRMGGAIIGRWYSYR 132

RESULT 10
US-09-252-991A-20531
; Sequence 20531, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:	NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:	AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

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Query Match          52.6%; Score 41; DB 4; Length 492;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 8; Conservative 3; Mismatches 1; Indels 4; Gaps 1;

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Qy 3 RLPKRMGGSY---RC 14
|||:|:|:|
Db 361 RLPRLGGDHPVPVC 376

RESULT 11
US-09-252-991A-18691
; Sequence 18691, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; REFERENCE: KATZ, O. RUBENFELD ET AL.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

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Query Match      52.6%; Score 41; DB 4; Length 511;
Best Local Similarity 63.6%; Pred. NO. 36;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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Qy 2 QRLPKRMGGSY 12

Db 492 KRLPKSGGSH 502

RESULT 12
US-09-252-991A-22588
; Sequence 22588, Application US/09252991A

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO

Query Match 52.6%; Score 41; DB 4; Length 556;
Best Local Similarity 63.6%; Pred. No. 40;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 RLPKRMGGSYR 13
|||:|:|:|
Db 420 RLPRLGGGQR 430

RESULT 13
US-09-252-991A-17469
; Sequence 17469, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

Query Match 52.6%; Score 41; DB 4; Length 595;
 Best Local Similarity 70.0%; Pred. NO. 43;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PKRMGGSYRC 14
| : | | | | |
Db 38 PRRSGGSARC 47

RESULT 14
US-09-252-991A-22757
Application US/09252991A

RESULTS
US-09-252-991A-22757
; Sequence 22757 Application US/09252991A

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22757
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22757

Query Match 51.3%; Score 40; DB 4; Length 303;
Best Local Similarity 57.1%; Pred. No. 31;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RQRLPKRMGGSYRC 14
| | | | : | | |
Db 61 RQRLRRRWSGRRRC 74

RESULT 15
US-09-252-991A-27426
; Sequence 27426, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27426
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27426

Query Match 51.3%; Score 40; DB 4; Length 355;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQRLPKRMGGSY 12
| : | : | : | : | :
Db 103 RRRVPDRLGGAH 114

Search completed: November 19, 2005, 01:59:10
Job time : 28 secs

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OM protein - protein search, using sw model

Run on: November 18, 2005, 00:29:25 ; Search time 73 Seconds
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Title: US-09-745-008-14
Perfect score: 78
Sequence: 1 RQRLPKRMGGSYRC 14

Scoring table: BLOSUM62
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Searched: 1867879 seqs, 418409474 residues

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Listing first 45 summaries

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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	78	100.0	14	9 US-09-745-008-14	Sequence 14, Appl
2	78	100.0	21	9 US-09-745-008-13	Sequence 13, Appl
3	78	100.0	1162	9 US-09-745-008-34	Sequence 34, Appl
4	67.5	86.5	45	9 US-09-745-008-12	Sequence 12, Appl
5	43	55.1	105	16 US-10-437-963-113983	Sequence 113983,
6	43	55.1	133	16 US-10-425-115-278836	Sequence 278836,
7	43	55.1	142	15 US-10-425-114-58669	Sequence 58669, A
8	43	55.1	155	15 US-10-425-114-51601	Sequence 51601, A
9	43	55.1	162	15 US-10-425-114-47458	Sequence 47458, A
10	43	55.1	164	15 US-10-425-114-39475	Sequence 39475, A
11	43	55.1	165	15 US-10-425-114-38751	Sequence 38751, A

12	43	55.1	165	15	US-10-425-114-44961	Sequence 44961, A
13	43	55.1	166	15	US-10-425-114-39600	Sequence 39600, A
14	43	55.1	166	15	US-10-425-114-60911	Sequence 60911, A
15	43	55.1	166	15	US-10-425-114-62444	Sequence 62444, A
16	43	55.1	169	15	US-10-425-114-67338	Sequence 67338, A
17	43	55.1	179	15	US-10-425-114-61006	Sequence 61006, A
18	43	55.1	179	15	US-10-425-114-62787	Sequence 62787, A
19	43	55.1	181	15	US-10-425-114-39542	Sequence 39542, A
20	43	55.1	181	15	US-10-425-114-72129	Sequence 72129, A
21	43	55.1	181	15	US-10-425-114-72143	Sequence 72143, A
22	43	55.1	183	15	US-10-425-114-58636	Sequence 58636, A
23	43	55.1	184	15	US-10-425-114-55429	Sequence 55429, A
24	43	55.1	185	15	US-10-425-114-47709	Sequence 47709, A
25	43	55.1	185	15	US-10-425-114-65756	Sequence 65756, A
26	42	53.8	30	10	US-09-933-767-1167	Sequence 1167, Ap
27	42	53.8	30	14	US-10-004-860-1167	Sequence 1167, Ap
28	42	53.8	30	14	US-10-023-282-1167	Sequence 175186,
29	42	53.8	326	16	US-10-437-963-175186	Sequence 32442, A
30	42	53.8	339	20	US-11-097-143-32442	Sequence 176745,
31	41	52.6	208	16	US-10-437-963-176745	Sequence 176745,
32	41	52.6	397	16	US-10-437-963-143589	Sequence 143589,
33	41	52.6	524	16	US-10-739-930-10355	Sequence 10355, A
34	41	52.6	564	15	US-10-369-493-585	Sequence 585, App
35	40.5	51.9	235	14	US-10-240-154-22	Sequence 22, Appl
36	40.5	51.9	748	16	US-10-437-963-115827	Sequence 115827,
37	40	51.3	53	16	US-10-437-963-183455	Sequence 183455,
38	40	51.3	60	15	US-10-424-599-176730	Sequence 176730,
39	40	51.3	63	16	US-10-425-115-284352	Sequence 284352,
40	40	51.3	147	15	US-10-424-599-152415	Sequence 152415,
41	40	51.3	150	14	US-10-156-761-10416	Sequence 10416, A
42	40	51.3	151	18	US-10-450-763-47114	Sequence 47114, A
43	40	51.3	185	15	US-10-425-114-60116	Sequence 60116, A
44	40	51.3	230	9	US-09-741-669-372	Sequence 372, App
45	40	51.3	230	15	US-10-282-122A-42769	Sequence 42769, A

ALIGNMENTS

RESULT 1
US-09-745-008-14
; Sequence 14, Application US/09745008
; Patent No. US20020137667A1
; GENERAL INFORMATION:
; APPLICANT: Chuenkova, Marina
; APPLICANT: Pereira, Miercio A.
; TITLE OF INVENTION: T. Cruze-Derived Neurotrophic Agents and
; TITLE OF INVENTION: Methods of Use Therefor
; FILE REFERENCE: 1322.1028-001
; CURRENT APPLICATION NUMBER: US/09/745,008
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/172,881
; PRIOR FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-745-008-14

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US-09-745-008-13
; Sequence 13, Application US/09745008
; Patent No. US20020137667A1
; GENERAL INFORMATION:
; APPLICANT: Chuenkova, Marina
; APPLICANT: Pereira, Miercio A.
; TITLE OF INVENTION: T. Cruzi-Derived Neurotrophic Agents and
; TITLE OF INVENTION: Methods of Use Therefor
; FILE REFERENCE: 1322.1028-001
; CURRENT APPLICATION NUMBER: US/09745,008
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/172,881
; PRIOR FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-745-008-13

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DB 1 RQRLPKRMGGSYRC 14

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; Patent No. US20020137667A1
; GENERAL INFORMATION:
; APPLICANT: Chuenkova, Marina
; APPLICANT: Pereira, Miercio A.
; TITLE OF INVENTION: T. Cruzi-Derived Neurotrophic Agents and
; TITLE OF INVENTION: Methods of Use Therefor
; FILE REFERENCE: 1322.1028-001
; CURRENT APPLICATION NUMBER: US/09745,008
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/172,881
; PRIOR FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Trypanosoma cruzi
US-09-745-008-34

Query Match 100.0%; Score 78; DB 9; Length 1162;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 379 RQRLPKRMGGSYRC 392

RESULT 4

US-09-745-008-12
; Sequence 12, Application US/09745008
; Patent No. US20020137667A1
; GENERAL INFORMATION:
; APPLICANT: Chuenkova, Marina
; APPLICANT: Pereira, Miercio A.
; TITLE OF INVENTION: T. Cruzi-Derived Neurotrophic Agents and
; TITLE OF INVENTION: Methods of Use Therefor
; FILE REFERENCE: 1322.1028-001

; CURRENT APPLICATION NUMBER: US/09745,008
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/172,881
; PRIOR FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-745-008-12

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Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DB 24 RQRLPKRMGGSYRC 38

RESULT 5

US-10-437-963-113983
; Sequence 113983, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
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; LENGTH: 105
; TYPE: PRT
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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_17719C.1.pep
US-10-437-963-113983

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Best Local Similarity 64.3%; Pred. No. 19;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 3 RLPK--RMGGSYRC 14
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DB 63 RLPRVSRSGGPYRC 76

RESULT 6

US-10-425-115-278836
; Sequence 278836, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326
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; LENGTH: 133
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_185877C.1.pep
US-10-425-115-278836

Query Match 55.1%; Score 43; DB 16; Length 133;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

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Db 107 QRCPGNRRRLGSLRC 121

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US-10-425-114-58669
; Sequence 58669, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
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; FEATURE:
; OTHER INFORMATION: Clone ID: 700615246_FLI.pep
US-10-425-114-58669

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Db 108 RRRLPRRLGG 117.

RESULT 8
US-10-425-114-51601
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; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 51601
; LENGTH: 155
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; ORGANISM: Zea mays

; FEATURE:
; OTHER INFORMATION: Clone ID: 700222827_FLI.pep
US-10-425-114-51601

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QY 1 RORLPKRMGG 10
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Db 133 RRRLPRRLGG 142

RESULT 9
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; Sequence 47458, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
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US-10-425-114-47458

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Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 133 RRRLPRRLGG 142

RESULT 10
US-10-425-114-39475
; Sequence 39475, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 39475
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; ORGANISM: Zea mays
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; OTHER INFORMATION: Clone ID: 700207896_FLI.pep
US-10-425-114-39475

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Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 108 RRRLPRRLGG 117

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; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
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; ORGANISM: Zea mays
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US-10-425-114-38751

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Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 108 RRRLPRRLGG 117

RESULT 12
US-10-425-114-44961
; Sequence 44961, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
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; ORGANISM: Zea mays
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; OTHER INFORMATION: Clone ID: 700448317_FLI.pep
US-10-425-114-44961

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Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 108 RRRLPRRLGG 117

RESULT 13
US-10-425-114-39600
; Sequence 39600, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
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; ORGANISM: Zea mays
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US-10-425-114-39600

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Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 108 RRRLPRRLGG 117

RESULT 14
US-10-425-114-60911
; Sequence 60911, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 60911
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3354-104-B1_FLI.pep
US-10-425-114-60911

Query Match 55.1%; Score 43; DB 15; Length 166;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRLPKRMGG 10
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Db 108 RRRLPRRLGG 117

RESULT 15
US-10-425-114-62444

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; Sequence 62444, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62444
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; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700578933_FLI.pep
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Best Local Similarity 70.0%; Pred. No. 31;
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